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Original Article

Prevalence and Molecular Aspects of Human Hookworms in Guilan Province, Northern Iran

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Abstract

Background: Hookworm infection is one of the important Neglected Tropical Diseases (NTD) in the world. It was previously more prevalent in the northern and southern parts of Iran with a prevalence rate higher than 40% in some endemic regions; nevertheless, the infection rate has decreased to less than 1%. This study aimed to determine prevalence and molecular aspects of hookworm infections in rural inhabitants of Fouman County, Guilan Province, northern Iran

Methods: This cross-sectional study was performed in 31 villages of Fouman district in Guilan Province, northern Iran during 2015-2016. Stool samples were collected from 1500 rural inhabitants and examined by formalin ethyl-acetate concentration as well as agar plate culture techniques. After treatment with albendazole, adult hookworms were isolated. Following DNA extraction, PCR amplification of ITS2-rDNA region was performed and the product was sequenced, followed by genetic variation analysis.

Results: Of 1500 samples, one case was morphologically diagnosed as *N. americanus*. In addition, molecular characterization verified the presence of *N. americanus,* showing more than 95% similarity with sequences of *N. americanus* present in GenBank. The patient showed no clinical symptoms and a mild hypereosinophilia was the only laboratory finding observed.

Conclusion: A reduced prevalence of human hookworms was demonstrated within Guilan Province located in north of Iran. The *N. americanus* originated from Guilan had a high homology with the isolates found in Japan, Laos, Malaysia, and Australia.